

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Evans, Ronald M.  
Forman, Barry M.
- 5 (ii) TITLE OF INVENTION: SELECTIVE MODULATORS OF PEROXISOME  
PROLIFERATOR ACTIVATED RECEPTOR-GAMMA, AND METHODS FOR THE USE  
THEREOF
- (iii) NUMBER OF SEQUENCES: 6
- 10 (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
(B) STREET: 444 South Flower Street, Suite 2000  
(C) CITY: Los Angeles  
(D) STATE: CA  
15 (E) COUNTRY: USA  
(F) ZIP: 90071
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
20 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/465,375  
(B) FILING DATE: 05-JUN-1995  
25 (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/428,559  
(B) FILING DATE: 25-APR-1995
- 30 (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Reiter, Stephen E.  
(B) REGISTRATION NUMBER: 31,192  
(C) REFERENCE/DOCKET NUMBER: P41 90001
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 619-546-1995  
35 (B) TELEFAX: 619-546-9392

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2005 base pairs  
40 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
(A) NAME/KEY: CDS  
45 (B) LOCATION: 352..1776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATCGAATCCC GCGCCCCAGG CGCTGCCGCT CTGAGTGCGA CGGGCCCCGC CTGGCCGGCC

	GGAGGACGCG	GAAGAAGAGA	CCTGGGGCGC	TGCCTGGGGT	ATTGGGTCGC	GCGCAGTGAG	120
	GGGACCGAGT	GTGACGACAA	GGTGACCGGG	CTGAGGGGAC	GGGCTGAGGA	GAAGTCACAC	180
	TCTGACAGGA	GCCTGTGAGA	CCAACAGCCT	GACGGGGTCT	CGGTTGAGGG	GACGCGGGCT	240
	GAGAAGTCAC	GTTCTGACAG	GACTGTGTGA	CAGACAAGAT	TTGAAAGAAG	CGGTGAACCA	300
5	CTGATATTCA	GGACATTTTT	AAAAACAAGA	CTACCCTTTA	CTGAAATTAC	C ATG GTT Met Val 1	357
10	GAC ACA GAG ATG CCA TTC TGG CCC ACC AAC TTC GGA ATC AGC TCT GTG Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val	5	10	15			405
	GAC CTC TCC GTG ATG GAA GAC CAC TCG CAT TCC TTT GAC ATC AAG CCC Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro	20	25	30			453
15	TTT ACC ACA GTT GAT TTC TCC AGC ATT TCT GCT CCA CAC TAT GAA GAC Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Ala Pro His Tyr Glu Asp	35	40	45	50		501
	ATT CCA TTC ACA AGA GCT GAC CCA ATG GTT GCT GAT TAC AAA TAT GAC Ile Pro Phe Thr Arg Ala Asp Pro Met Val Ala Asp Tyr Lys Tyr Asp	55	60	65			549
20	CTG AAG CTC CAA GAA TAC CAA AGT GCG ATC AAA GTA GAA CCT GCA TCT Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser	70	75	80			597
25	CCA CCT TAT TAT TCT GAA AAG ACC CAG CTC TAC AAC AGG CCT CAT GAA Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Arg Pro His Glu	85	90	95			645
	GAA CCT TCT AAC TCC CTC ATG GCC ATT GAG TGC CGA GTC TGT GGG GAT Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp	100	105	110			693
30	AAA GCA TCA GGC TTC CAC TAT GGA GTT CAT GCT TGT GAA GGA TGC AAG Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys	115	120	125	130		741
	GGT TTT TTC CGA AGA ACC ATC CGA TTG AAG CTT ATT TAT GAT AGG TGT Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys	135	140	145			789
35	GAT CTT AAC TGC CGG ATC CAC AAA AAA AGT AGA AAT AAA TGT CAG TAC Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr	150	155	160			837
40	TGT CGG TTT CAG AAG TGC CTT GCT GTG GGG ATG TCT CAC AAT GCC ATC Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala Ile	165	170	175			885
	AGG TTT GGG CGG ATG CCA CAG GCC GAG AAG GAG AAG CTG TTG GCG GAG Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu	180	185	190			933
45	ATC TCC AGT GAT ATC GAC CAG CTG AAC CCA GAG TCT GCT GAT CTG CGA Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg	195	200	205	210		981
	GCC CTG GCA AAG CAT TTG TAT GAC TCA TAC ATA AAG TCC TTC CCG CTG Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro Leu	215	220	225			1029

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	ACC AAA GCC AAG GCG AGG GCG ATC TTG ACA GGA AAG ACA ACG GAC AAA	1077
	Thr Lys Ala Lys Ala Arg Ala Ile L u Thr Gly Lys Thr Thr Asp Lys	
	230 235 240	
5	TCA CCA TTT GTC ATC TAC GAC ATG AAT TCC TTA ATG ATG GGA GAA GAT	1125
	Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu Asp	
	245 250 255	
	AAA ATC AAG TTC AAA CAT ATC ACC CCC CTG CAG GAG CAG AGC AAA GAG	1173
	Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu	
	260 265 270	
10	GTG GCC ATC CGA ATT TTT CAA GGG TGC CAG TTT CGA TCC GTA GAA GCC	1221
	Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala	
	275 280 285 290	
15	GTG CAA GAG ATC ACA GAG TAT GCC AAA AAT ATC CCT GGT TTC ATT AAC	1269
	Val Gln Glu Ile Thr Glu Tyr Ala Lys Asn Ile Pro Gly Phe Ile Asn	
	295 300 305	
	CTT GAT TTG AAT GAC CAA GTG ACT CTG CTC AAG TAT GGT GTC CAT GAG	1317
	Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu	
	310 315 320	
20	ATC ATC TAC ACG ATG CTG GCC TCC CTG ATG AAT AAA GAT GGA GTC CTC	1365
	Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu	
	325 330 335	
	ATC TCA GAG GGC CAA GGA TTC ATG ACC AGG GAG TTC CTC AAA AGC CTG	1413
	Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu	
	340 345 350	
25	CGG AAG CCC TTT GGT GAC TTT ATG GAG CCT AAG TTT GAG TTT GCT GTG	1461
	Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val	
	355 360 370	
30	AAG TTC AAT GCA CTG GAA TTA GAT GAC AGT GAC TTG GCT ATA TTT ATA	1509
	Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile	
	375 380 385	
	GCT GTC ATT ATT CTC AGT GGA GAC CGC CCA GGC TTG CTG AAC GTG AAG	1557
	Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys	
	390 395 400	
35	CCC ATC GAG GAC ATC CAA GAC AAC CTG CTG CAG GCC CTG GAA CTG CAG	1605
	Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu Gln	
	405 410 415	
	CTC AAG CTG AAT CAC CCA GAG TCC TCT CAG CTG TTC GCC AAG GTG CTC	1653
	Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Val Leu	
	420 425 430	
40	CAG AAG ATG ACA GAC CTC AGG CAG ATC GTC ACA GAG CAC GTG CAG CTA	1701
	Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu	
	435 440 445 450	
45	CTG CAT GTG ATC AAG AAG ACA GAG ACA GAC ATG AGC CTT CAC CCC CTG	1749
	Leu His Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro Leu	
	455 460 465	
	CTC CAG GAG ATC TAC AAG GAC TTG TAT TAGCAGGAAA GTCCCACCCG	1796
	Leu Gln Glu Ile Tyr Lys Asp Leu Tyr	
	470 475	
	CTGACAACGT GTTCCTTCTA TTGATTGCAC TATTATTTTG AGGGAAAAAA ATCTGACACC	1856

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TAAGAAATTT	ACTGTGAAAA	AGCATTTAAA	AACAAAAAGT	TTTAGAACAT	GATCTATTTT	1916
ATGCATATTG	TTTATAAAGA	TACATTTACA	ATTTACTTTT	AATATTAAAA	ATTACCACAT	1976
TATAAAAAAA	AAAAAAAAAA	AGGAATTCC				2005

(2) INFORMATION FOR SEQ ID NO:2:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 546 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

- 10 (ii) MOLECULE TYPE: cDNA

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(ix) FEATURE:
      (A) NAME/KEY: CDS
      (B) LOCATION: 35..544
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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

|    |            |            |            |      |     |     |     |     |     |     |     |     |     |     |     |     |  |     |
|----|------------|------------|------------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| 15 | GGGAGACCCA | AGCTTGAAGC | AAGCCTCCTG | AAAG | ATG | CTA | CTG | TCT | TCT |     |     |     |     |     |     |     |  | 52  |
|    |            |            |            |      | Met | Lys | Leu | Leu | Ser | Ser |     |     |     |     |     |     |  |     |
|    |            |            |            |      | 1   |     |     |     |     |     |     |     |     |     | 5   |     |  |     |
| 20 | ATC        | GAA        | CAA        | GCA  | TGC | GAT | ATT | TGC | CGA | CTT | AAA | AAG | CTC | AAG | TGC | TCC |  | 100 |
|    | Ile        | Glu        | Gln        | Ala  | Cys | Asp | Ile | Cys | Arg | Leu | Lys | Lys | Leu | Lys | Cys | Ser |  |     |
|    |            |            |            | 10   |     |     |     |     | 15  |     |     |     |     |     | 20  |     |  |     |
|    | AAA        | GAA        | AAA        | CCG  | AAG | TGC | GCC | AAG | TGT | CTG | AAG | AAC | AAC | TGG | GAG | TGT |  | 148 |
|    | Lys        | Glu        | Lys        | Pro  | Lys | Cys | Ala | Lys | Cys | Leu | Lys | Asn | Asn | Trp | Glu | Cys |  |     |
|    |            |            |            | 25   |     |     |     | 30  |     |     |     |     |     | 35  |     |     |  |     |
| 25 | CGC        | TAC        | TCT        | CCC  | AAA | ACC | AAA | AGG | TCT | CCG | CTG | ACT | AGG | GCA | CAT | CTG |  | 196 |
|    | Arg        | Tyr        | Ser        | Pro  | Lys | Thr | Lys | Arg | Ser | Pro | Leu | Thr | Arg | Ala | His | Leu |  |     |
|    |            | 40         |            |      |     |     | 45  |     |     |     |     | 50  |     |     |     |     |  |     |
|    | ACA        | GAA        | GTG        | GAA  | TCA | AGG | CTA | GAA | AGA | CTG | GAA | CAG | CTA | TTT | CTA | CTG |  | 244 |
|    | Thr        | Glu        | Val        | Glu  | Ser | Arg | Leu | Glu | Arg | Leu | Glu | Gln | Leu | Phe | Leu | Leu |  |     |
|    |            | 55         |            |      |     | 60  |     |     |     |     | 65  |     |     |     |     | 70  |  |     |
| 30 | ATT        | TTT        | CCT        | CGA  | GAA | GAC | CTT | GAC | ATG | ATT | TTG | AAA | ATG | GAT | TCT | TTA |  | 292 |
|    | Ile        | Phe        | Pro        | Arg  | Glu | Asp | Leu | Asp | Met | Ile | Leu | Lys | Met | Asp | Ser | Leu |  |     |
|    |            |            |            |      | 75  |     |     |     |     | 80  |     |     |     |     | 85  |     |  |     |
|    | CAG        | GAT        | ATA        | AAA  | GCA | TTG | TTA | ACA | GGA | TTA | TTT | GTA | CAA | GAT | AAT | GTG |  | 340 |
|    | Gln        | Asp        | Ile        | Lys  | Ala | Leu | Leu | Thr | Gly | Leu | Phe | Val | Gln | Asp | Asn | Val |  |     |
|    |            |            |            | 90   |     |     |     |     | 95  |     |     |     |     | 100 |     |     |  |     |
| 35 | AAT        | AAA        | GAT        | GCC  | GTC | ACA | GAT | AGA | TTG | GCT | TCA | GTG | GAG | ACT | GAT | ATG |  | 388 |
|    | Asn        | Lys        | Asp        | Ala  | Val | Thr | Asp | Arg | Leu | Ala | Ser | Val | Glu | Thr | Asp | Met |  |     |
|    |            |            |            | 105  |     |     |     | 110 |     |     |     |     | 115 |     |     |     |  |     |
| 40 | CCT        | CTA        | ACA        | TTG  | AGA | CAG | CAT | AGA | ATA | AGT | GCG | ACA | TCA | TCA | TCG | GAA |  | 436 |
|    | Pro        | Leu        | Thr        | Leu  | Arg | Gln | His | Arg | Ile | Ser | Ala | Thr | Ser | Ser | Ser | Glu |  |     |
|    |            |            |            | 120  |     |     | 125 |     |     |     |     | 130 |     |     |     |     |  |     |
|    | GAG        | AGT        | AGT        | AAC  | AAA | GGT | CAA | AGA | CAG | TTG | ACT | GTA | TCG | CCG | GAA | TTC |  | 484 |
|    | Glu        | Ser        | Ser        | Asn  | Lys | Gly | Gln | Arg | Gln | Leu | Thr | Val | Ser | Pro | Glu | Phe |  |     |
|    |            |            |            |      |     | 140 |     |     |     |     | 145 |     |     |     | 150 |     |  |     |
| 45 | CCG        | GGG        | ATC        | CGT  | CGA | CGG | TAC | CAG | ATA | TCA | GGA | TCC | TGG | CCA | GCT | AGC |  | 532 |
|    | Pro        | Gly        | Ile        | Arg  | Arg | Arg | Tyr | Gln | Ile | Ser | Gly | Ser | Trp | Pro | Ala | Ser |  |     |
|    |            |            |            |      | 155 |     |     |     |     | 160 |     |     |     |     | 165 |     |  |     |

[illegible]

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TAG GTA GCT AGA GG  
 \* Val Ala Arg  
 170

546

## (2) INFORMATION FOR SEQ ID NO:3:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 170 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Lys Leu Leu Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu  
 1 5 10 15  
 Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu  
 20 25 30  
 15 Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro  
 35 40 45  
 Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu  
 50 55 60  
 20 Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile  
 65 70 75 80  
 Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu  
 85 90 95  
 Phe Val Gln Asp Asn Val Asn Lys Asp Ala Val Thr Asp Arg Leu Ala  
 100 105 110  
 25 Ser Val Glu Thr Asp Met Pro Leu Thr Leu Arg Gln His Arg Ile Ser  
 115 120 125  
 Ala Thr Ser Ser Ser Glu Glu Ser Ser Asn Lys Gly Gln Arg Gln Leu  
 130 135 140  
 30 Thr Val Ser Pro Glu Phe Pro Gly Ile Arg Arg Arg Tyr Gln Ile Ser  
 145 150 155 160  
 Gly Ser Trp Pro Ala Ser \* Val Ala Arg  
 165 170

## (2) INFORMATION FOR SEQ ID NO:4:

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 13 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

## 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGGACAAAGG TCA

13

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31

## (2) INFORMATION FOR SEQ ID NO:5:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both
- (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGACCAGGAC AAAGGTCACG TTC

23

## 10 (2) INFORMATION FOR SEQ ID NO:6:

- 15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both
- (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGGAGGACTG TCCTCCG

17

09155252.092108  
00T260"2525T60